UNITED STATES DEPARTMENT OF COMMERCE
National Oceanic and Atmospheric Administration
NATIONAL MARINE FISHERIES SERVICE
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MEMORANDUM

Date: December 23, 2005
From: Tom Cooney, Michelle McClure and the Interior Columbia Technical Recovery Team
To: NMFS NW Regional Office, Co-managers and other interested parties
Subject: Updates to ESU/Population Viability Criteria for the Interior Columbia Basin

Introduction

The Interior Columbia Technical Recovery Team released its draft document, establishing viability goals at the population, Major Population Group (MPG) and ESU level, in July 2005 (IC-TRT, 2005). This memo provides an update of changes and additions to these criteria. We release this update for use in the local recovery planning process, and in other recovery-relevant processes, such as the development of the FCRPS Biological Opinion. We include here four specific changes and additions:

1. Additions to the text of our genetic metric, B.1.c, (which contributes to an overall spatial structure and diversity rating), clarifying the conditions under which populations with ‘moderate’ or ‘high’ risk ratings can receive a lower risk rating.
2. Clarification to our spawner composition metric, B.2.a, providing greater guidance about the total proportion of hatchery spawners associated with risk levels.
3. Updates to population size category analyses and revised ESU summary tables.
4. Expanded discussion regarding addressing uncertainty in abundance/productivity measures.
5. Adaptations to population level criteria (viability curve and spatial structure/diversity measures) for application to Snake River fall chinook.

Genetic Metric B.1.c. – Additions to text

Our genetic metric, B.1.c is describes population-level genetic characteristics consistent with varying risk levels. It became clear while working with local recovery planners and NOAA staff populations that had been perturbed genetically (e.g. had allele frequencies statistically indistinguishable from an out-of-ESU hatchery stock) posed a particular challenge. Specifically, identifying those situations in which the risk could be considered to have been reduced from the original perturbation was unclear. Below, we reproduce our genetic criterion, but provide also additional information guiding the assignment of risk ratings in these situations. New text is italicized.

New text for Factor B.1.c.

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New text for Factor B.1.c.

Factor B.1.c. Genetic variation. This factor addresses observed changes in genetic variation, regardless of the cause of that change (e.g., whether the change is due to introgression from non-local hatchery spawners or from the adverse genetic consequences of small population size).

We recommend that current and past population-specific genetic data sets be evaluated for:

- the amount of genetic variation detected within the population or subpopulations;
- the level of differentiation between subcomponents of the population;
- the level of differentiation between the population and other populations (including hatchery stocks); and,
- temporal change in levels of variation or differentiation within and between populations.

These characteristics may be expressed by such measures as statistically significant reductions in heterozygosity, number of alleles, changes in allele frequencies, presence of non-native alleles, or as among locus (gametic) or within locus (genotypic) disequilibria consistent with ongoing or recent admixture with non-native populations.

However, we do not include specific genetic metrics or cutoffs in our criteria for three reasons. Most importantly, the wide variety of circumstances in the interior Columbia Basin requires a case-by-case examination of genetic data. For instance, available baseline genetic information may not be a reasonable picture of natural levels of genetic variation due to bottlenecks the population has experienced, or to extreme introgression from hatchery fish. Therefore, in some cases, change from a baseline might reduce the apparent risk to a population, whereas in others, the same degree of change might constitute a significant increase in risk level. Second, the ever-changing nature of molecular genetic techniques and analyses suggests that new advances may provide additional or improved methods to measure genetic variation. Finally, degree or magnitude of differentiation that could be gauged to be "high" or "low" will vary between species and data type and quality.

We do suggest risk levels associated with degree of change from "actual or presumed historical conditions" for genetic characteristics (Table 11). Requiring populations to show low levels of change from "actual or presumed historical conditions" is not meant to imply that the population must have the precise distribution of alleles that it had historically. Rather, we mean that the general pattern of differentiation exhibited within and between populations should be similar to that which existed historically (if a suitable baseline exists) or that which can be inferred as being likely from similar populations populations where reliable genetic inferences have been made.

Two issues relevant to categorizing a population with respect to this genetic criterion are worth particular mention. The first is the relatively slow response of neutral genetic markers to genetic drift. Thus, populations that have been homogenized with each other, or with a hatchery stock, will not, if they maintain relatively large population sizes, show levels of differentiation consistent with those that existed historically in short time scales. In these situations, analyses that can be used to assess whether the population merits a risk rating lower than is immediately apparent from its genetic characteristics include:

- *a fine-scale genetic analysis indicating that substructure within the population exists (i.e. that fish spawning in geographic proximity also show greater genetic affinity than they do to fish spawning more distantly). This structure should be confirmed across the population, and not be confined to a small portion. In addition, a sufficient number of generations to ensure high confidence in the results should be included;*
- *an analysis of genetic data indicating that the amount of divergence seen, even if differences between populations are not significant, is consistent with the time since the cessation of the perturbation and a very low level of exchange between populations. This analysis must include several samples both within and among the populations of interest;*
- *a robust analysis of patterns of dispersal. This would include sufficient spatial and temporal coverage to have high confidence that the population is neither receiving or distributing out-of-population spawners at a rate that is above the expected frequency in natural situations. An analysis of this type is inferential with respect to our genetic criterion, and should thus be invoked with caution.*

These analyses would be relevant for evaluating the characteristics of populations in the following management scenarios: re-introductions, re-building after population bottlenecks, and re-establishment of natural populations after an unnatural homogenizing event, such as overwhelming the population with hatchery-origin spawners.

Table 11. Factor B.1.c. Preliminary criteria describing risk levels associated with change in patterns of genetic variation.

Factor	Pop. Group	Risk Level			
		Very Low	Low	Moderate	High
Factor: Genetic variation Metric: Genetic analysis encompassing within and between population variation	A	No change from actual or presumed historical conditions	No change from actual or presumed historical conditions or evidence for a consistent trend towards historical conditions	Low level of change from actual or presumed historical conditions or evidence for a consistent trend towards historical conditions	Moderate or greater level of change from actual or presumed historical conditions
	B	No change from actual or presumed historical conditions	Low level of change from actual or presumed historical conditions or evidence for a consistent trend towards historical conditions	Moderate level of change from actual or presumed historical conditions or evidence for a trend towards historical conditions	Significant change from actual or presumed historical conditions
	C,D	No change from actual or presumed historical conditions	Criteria for A or B populations, dependent upon number of MSAs in population	Criteria for A or B populations, dependent upon number of MSAs in population	Criteria for A or B populations, dependent upon number of MSAs in population

<u>Spawner composition metric B.2.a – Clarifications</u>

Our spatial structure and diversity metrics also include an assessment of the proportion of exogenous spawners within a population, using a decision tree framework. However, as laid out, this metric leaves a small loophole, allowing populations with a high overall fraction of exogenous spawners, but low levels of those spawners from each of several sources to achieve a lower risk rating than is appropriate. Below, we reproduce our spawner composition criterion, with clarifying text in italics.

New text for factor B.2.a

Factor B.2.a. Spawner composition.

Natural breeding groups of Pacific salmon and trout (*Oncorhynchus* spp.) tend towards maintenance at natal localities because of strong homing capabilities coupled with localized adaptations (Hendry et al. 1998, 1999, NRC 1996, Reisenbichler et al. 2003). Stability of such aggregates over generations through centuries, and as fine as the local reach (Gharrett and Smoker 1993, Bentzen et al. 2001), is influenced by numbers of returning natal individuals (Waples 2004), ecological variability (Montgomery and Bolton 2003), and gene flow from exogenous fish (Utter 2001). This spatial and potentially adaptive level of variability within and between populations is recognized as important and necessary for viability of salmonid populations (McElhany et al. 2000). The stability of salmonid population structure can be undermined by effective straying resulting from returning hatchery releases and natural-origin strays induced by anthropogenically altered conditions. Such increases of gene flow above natural levels are counterproductive to recovery efforts within listed ESUs because of hatchery adaptations or domestication (Epifanio et al. 2003, Waples and Drake 2004), losses of genetic variability through supportive breeding (Ryman and Laikre 1991, Wang and Ryman 2001), and erosions of natural population structure such as homogenization (Utter 2005). The ultimate impact of these increases in gene flow is dependent upon the duration of the increase, the proportion of spawners that are not part of the normal system, and the origin of those spawners.

For this metric, we consider exogenous spawners to be all fish of hatchery-origin AND all natural-origin fish that are present due to unnatural, anthropogenically-induced conditions, but would not normally be present within the population. Upriver steelhead straying into the Deschutes River as an apparent result of unnatural high temperatures in the John Day reservoir would be one candidate for this category.

We have developed a flow-chart approach to assigning risk associated with exogenous spawners in salmonid populations (Figure 3). *Our approach is sequential, and evaluators should consider exogenous spawners in their population in the sequence laid out*. Our approach considers the source of the exogenous spawners first, providing increasing tolerance for both proportion and duration of exogenous spawners the more closely related they are to the population of interest. For exogenous spawners derived from the local population, we then consider the type of hatchery program from which those spawners were derived, allowing greater input from hatcheries using "best management practices. We do not specify specific management practices, because current and ongoing research will increase our understanding of the impact of hatchery operations and techniques on fitness characteristics. Rather we suggest that hatchery programs that conform to the principles described in recent publications (e.g. (Flagg et al. 2004, Olson et al. 2004, Mobrand et al. 2005) could be considered to have "best management practices." Main components of the program to be considered include broodstock selection, efforts to minimize within-population homogenization, actions to prevent domestication or other in-hatchery selection, breeding protocols, *rearing and release protocols* and other efforts to minimize effects on population structure and fitness components. Future assessments should consider advancements and updates in hatchery science when determining which category a particular program should be ascribed to.

These criteria are generally consistent with other efforts to quantify *risk from hatchery origin spawners (*e.g. Mobrand et al. 2005). However, we do encourage case-by-case treatment of conditions that may affect the risk experienced by the population. For instance, if exogenous spawners are localized within a large, complex population, leaving the bulk of the population unaffected, a somewhat higher proportion and/or duration of those exogenous spawners could be associated with a lower risk level. Similarly, in a very diverse MPG, the presence of exogenous spawners derived from a highly divergent population might merit higher risk levels than shown. While we offer this flexibility, such situations should be well-documented and justified.

There are several more detailed considerations for applying our criteria. First, when assessing the current status of a population, conditions in the most recent three generations should be considered. Second, the proportion of spawners belonging to a category should be calculated using the total number of spawners in the denominator.

Third, if there are multiple sources of exogenous spawners within a single population, *the total proportion of exogenous spawners should be considered. In general,* the highest risk level assigned to any of those sources should be used for this metric, unless there are two or more "moderate" rated sources, in which case a risk level of "high" should be used. *However, there may be situations where spawners from each source would yield individually a low rating, but the total proportion of exogenous spawners is relatively high. In these cases, the risk rating should be increased appropriately to either moderate or high.* Finally, we do not extend our criteria beyond 5 generations for any source of exogenous spawners, because there is considerable uncertainty about the long-term impacts of this unnatural gene flow. We anticipate that future research will allow these criteria to consider longer time periods more robustly.

This metric offers the opportunity to contribute to planning efforts as well as to evaluate current risk. Conservation and/or supplementation programs may be desirable to mitigate short-term extinction risk, for example. In these cases, this metric provides a transparent means to plan and coordinate recovery efforts to minimize the risks from such a program.

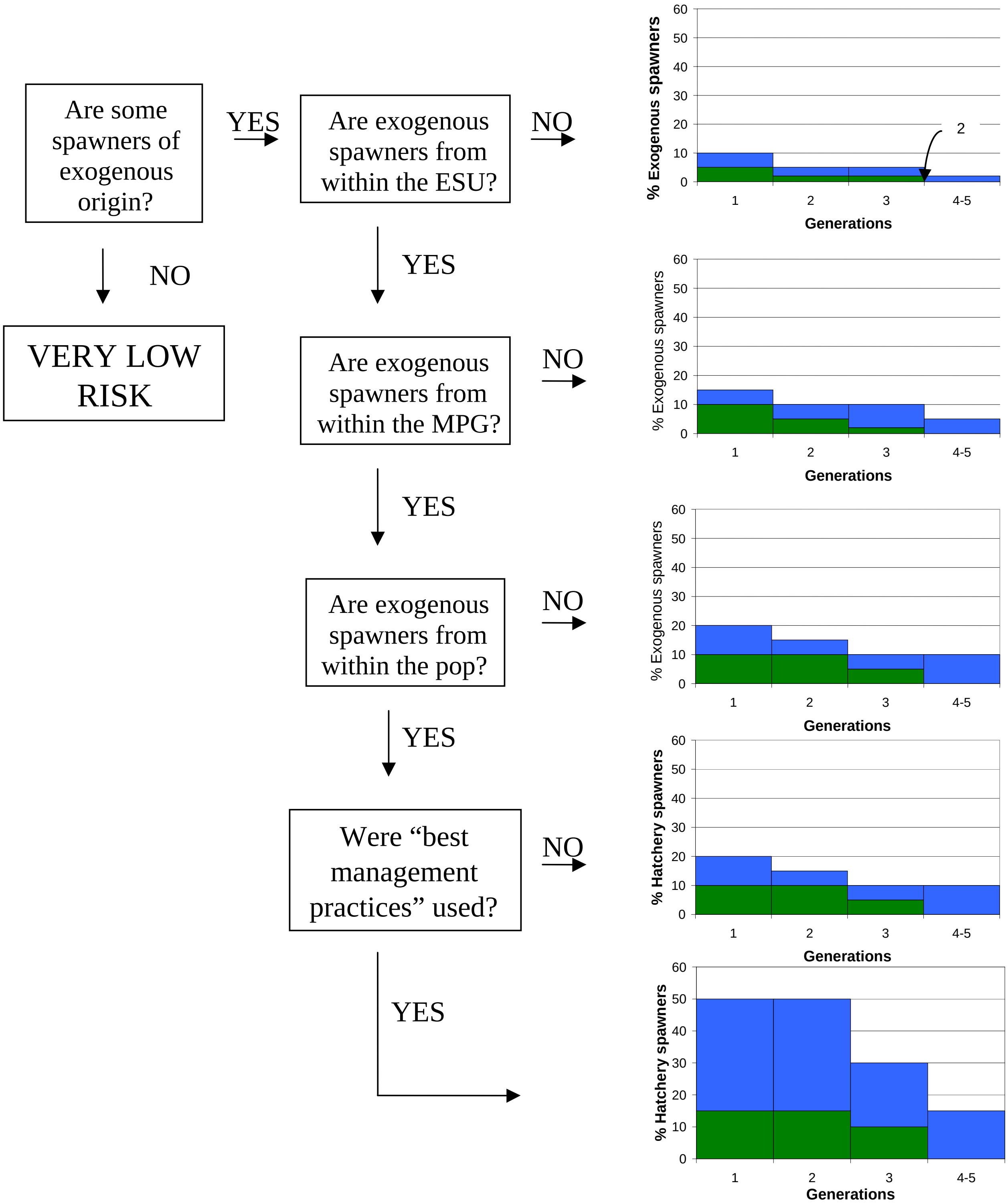


Figure 3. Graphical representation of risk criteria associated with spawner composition. Green (darkest) areas indicate low risk combinations of duration and proportion of spawners, blue (intermediate) areas indicate moderate risk areas and white areas and areas outside the range graphed indicate high risk. Exogenous fish are considered to be all fish of hatchery origin, and non-normative strays of natural origin (see text).

<u>Population size categories</u>

As a general rule of thumb, the ICTRT linked small downstream tributaries capable of supporting some level of spawning and rearing with the nearest upstream core production area. In the July draft, the ICTRT used the total amount of habitat (based on intrinsic potential analysis) to put populations into discrete categories - basic, intermediate, large and very large. This update includes revised summary tables and figures summarizing population size category assignments for each ESU. The population size categories are used in determining Major Population Group viability requirements and in application of spatial structure and diversity criteria.

We have included revised tables and figures including the changes in size category assignments for spring/summer chinook and steelhead populations in this update. The revised tables also include corrections and updates to the number of historical spawning areas associated with each population. We have amended our approach for assigning population specific abundance thresholds to emphasize the core area for each population - the major drainage or aggregate of major spawning areas.

The attached tables (3 a-f) include revised historical habitat estimates (in terms of weighted intrinsic potential). The assignment of relative population size to the amount of historical habitat within core areas shifted the threshold for application to four steelhead populations. The Umatilla population threshold was reduced to 1500 and the minimum abundance threshold for Asotin Creek, Little Salmon River and Chamberlain Creek has been reduced to 500 based on the estimated size of their respective core spawning drainages.

Table 1. (revised 12/23/05) Minimum abundance thresholds by species and historical population size (spawning area) for Interior Columbia Basin stream type chinook and steelhead populations (Table 3). Median weighted area and corresponding spawners per km (calculated as ratio with corresponding threshold) provided for populations in each size category (see attachment B).

Population Size Category	**Stream Type Chinook** (Upper Columbia Spr, Snake Spr/Sum ESUs)			**Steelhead** (Upper Columbia, Middle Columbia & Snake River ESUs)		
	Threshold	**Median Weighted Area (m X 10,000)**	**Spawners per KM (weighted)**	**Threshold**	**Median Weighted Area (m X 10,000)**	**Spawners per KM (weighted)**
Basic	***500***	22	22.7	***500***	105	4.8
Intermediate	***750***	44	17.0	***1,000***	309	3.2
Large	***1,000***	69	14.5	***1,500***	623	2.4
Very Large	***2,000***	145	13.8	***2,250***	923	2.4

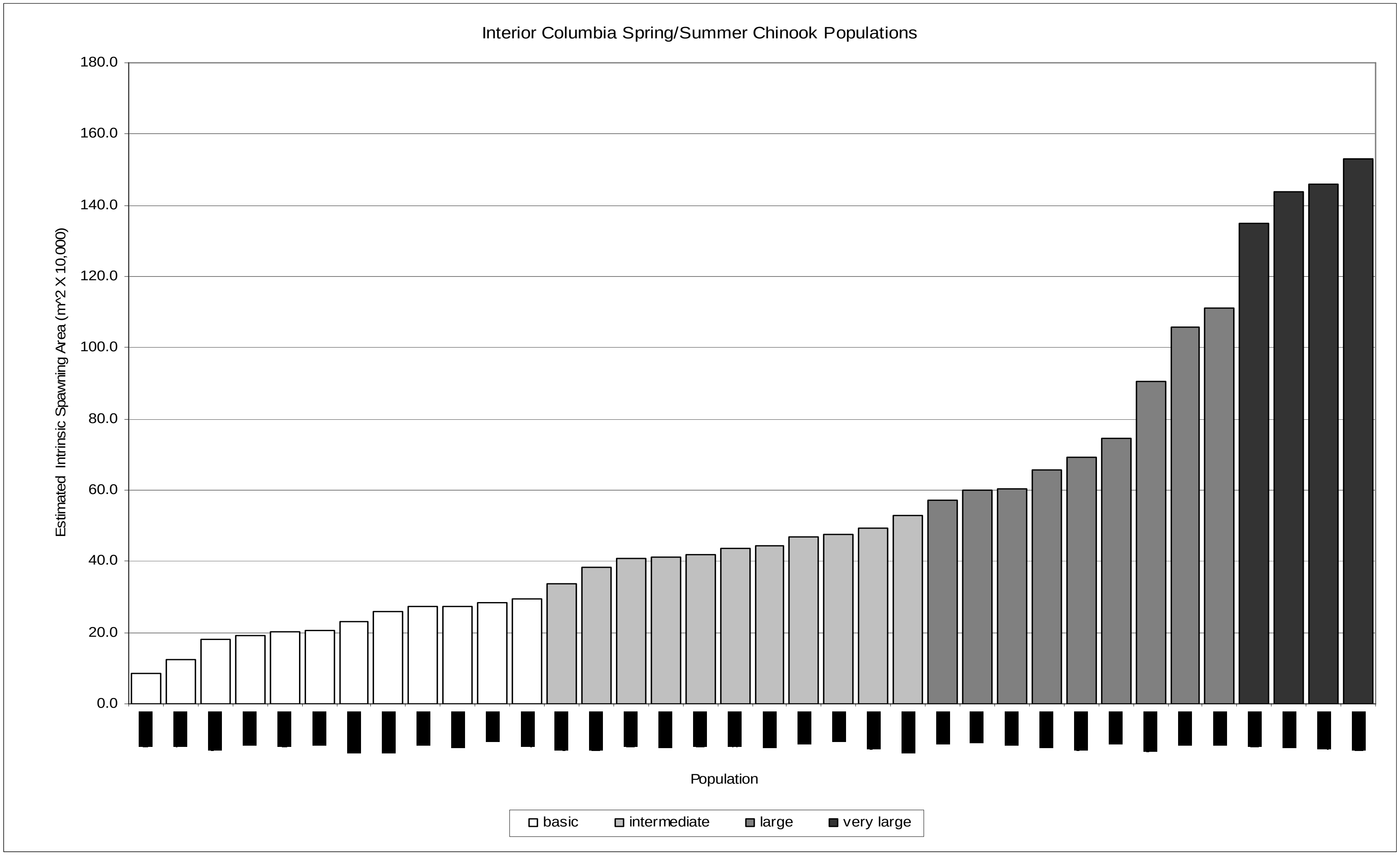
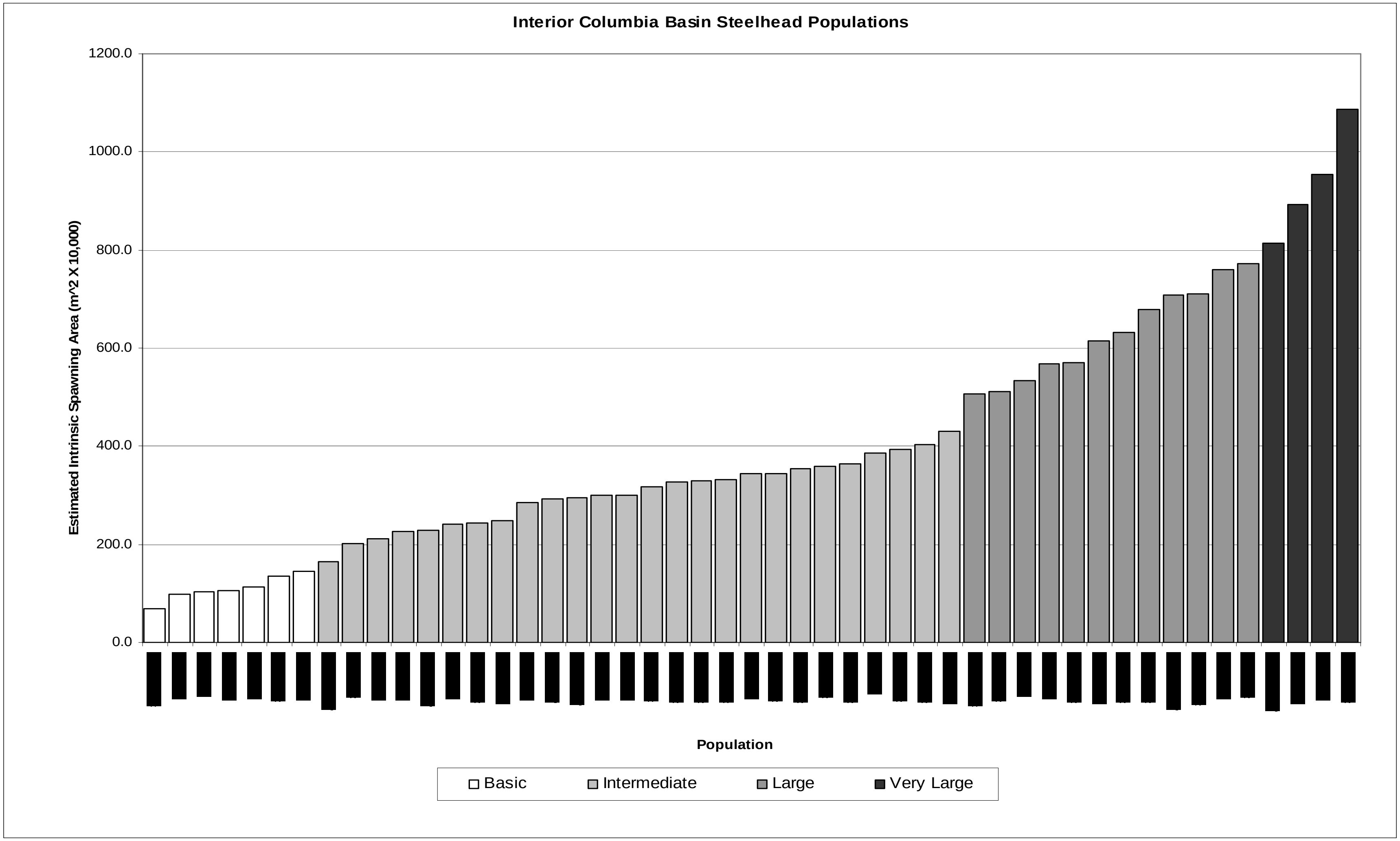


Figure 1 Attachment B). Revised 12/16/05. The East Fork South Fork Salmon River population has moved from intermediate to large (change due to updated barrier info). Note that the abundance thresholds for two Intermediate populations, Chamberlain and Little Salmon River, are reduced to 500 based on the relative size of their core drainage areas.



*These populations have adjusted abundance thresholds reflecting the size of their respective core drainage spawning areas.
**The size of these populations accounts for extirpated areas within extant populations.

Figure 2 (Attachment B) Revised 12/16/05. Size category ratings for interior Columbia Steelhead populations.

Table 3.a: Intrinsic size and complexity ratings for **extant Snake River Spring Chinook ESU** populations organized by Major Population Groupings. Complexity categories: A Simple linear; B=Dendritic; C= trellis pattern; D= core drainage plus adjacent but separate small tributaries. Underlined entries represent a change from the previous designation. Size categories in parentheses represent core tributary production areas.

Major Population Group	**Population**	**Weighted Area Category**	**Complexity**	
			Category	**#MaSAs/ (#MiSAs)**
Lower Snake	Tucannon R	Intermediate	D	1 (1)
	Asotin R.	Basic	A	0 (1)
Grande Ronde/Imnaha R	Lostine/Wallowa R.	Large	B	3 (1)
	Upper Grande Ronde R.	Large	B	3 (1)
	Catherine Creek	Large	B	3 (2)
	Imnaha R. Mainstem	Intermediate	A	1 (1)
	Minam R.	Intermediate	A	1
	Wenaha R.	Intermediate	A	1
	Big Sheep Cr.	Basic	A	0 (1)
	Lookingglass Cr.	Basic	A	0 (1)
South Fork Salmon	South Fk Mainstem	Large	C	2 (2)
	Secesh R.	Intermediate	A	1 (1)
	East Fk/Johnson Cr.	Large	B	1
	Little Salmon R.	Inter. (Basic)	D	0 (3)
Middle Fork Salmon	Big Creek	Large	B	3
	Bear Valley	Intermediate	C	3
	Upper Mainstem MF	Intermediate	C	1 (2)
	Chamberlain Cr.	Inter. (Basic)	D	1 (3)
	Camas Creek	Basic	B	1 (1)
	Loon Creek	Basic	C	1
	Marsh Creek	Basic	C	1
	Lower Mainstem MF	Basic	A	0 (1)
	Sulphur Creek	Basic	A	1
Upper Salmon	Lemhi	Very Large	B	3 (2)
	Lower Mainstem	Very Large	C	3 (1)
	Pahsimeroi	Large	B	1
	Upper Salmon East Fk	Large	C	1
	Upper Salmon Mainstem	Large	C	3
	Panther Cr (ext)	Intermediate		
	Valley Cr.	Basic	A	1
	Yankee Fork	Basic	C	1
	North Fork Salmon R.	Basic	D	1

Table 3.b: Intrinsic size and complexity ratings for historical **Snake River Steelhead ESU** populations organized by Major Population Groupings. Complexity categories: A = Simple linear; B=Dendritic; C= trellis pattern; D= core drainage plus adjacent but separate small tributaries. Underlined entries represent a change from the previous designation. Size categories in parentheses represent core tributary production areas.

Major Population Group	**Population**	**Weighted Area Category**	**Complexity**	
			Category	**#MaSAs/ (#MiSAs)**
Lower Snake	Tucannon R	Intermediate	A	2 (8)
	Asotin R.	Inter. (Basic)	D	4 (10)
Grande Ronde	Upper Grand Ronde R.	Large	B	10 (8)
	Wallowa River	Intermediate	B	6 (1)
	Lower Grande Ronde R.	Intermediate	B	4 (10)
	Joseph Creek	Intermediate	B	2 (0)
Imnaha R.	Imnaha River	Intermediate	B	4 (0)
Clearwater R.	Lower Mainstem	Large	B	5 (13)
	Selway River	Large	B	9 (7)
	South Fork	Intermediate	B	4 (4)
	Lochsa River	Large	B	7 (5)
	Lolo Creek	Basic	C	1 (0)
	North Fork (blocked)	Very Large		
Salmon River	Lemhi	Intermediate	B	5 (4)
	Upper Salmon East Fk	Intermediate	B	3 (5)
	Upper Salmon Mainstem	Intermediate	B	5 (2)
	Upper Middle Fork	Large	B	7 (2)
	Lower Middle Fork	Large	B	6 (6)
	Chamberlain Cr.	Inter. (Basic)	D	3 (9)
	Pahsimeroi River	Intermediate	C	3 (5)
	Panther Cr	Intermediate	D	4 (1)
	Little Salmon River	Inter. (Basic)	D	5 (8)
	South Fork	Intermediate	B	3 (2)
	Secesh R.	Basic	C	2 (0)
	North Fork	Basic	D	1 (3)
Hells Canyon Tributaries	Wild Horse/Powder R.	Note: Core spawning areas for this population are blocked to anadromous migration.		

Table 3.c: Intrinsic size and complexity ratings for historical populations within the **MIDCOLUMBIA RIVER STEELHEAD ESU**. Organized by Major Population Groupings. Complexity categories: A = Simple linear; B=Dendritic; C= trellis pattern; D= core drainage plus adjacent but separate small tributaries. Underlined entries represent a change from the previous designation. Size categories in parentheses represent core tributary production areas.

Major Population Group	Population	Weighted Area Category	Complexity	
			Category	# MaSA (# MiSA)
Eastern Cascades	Deschutes (westside)	Large (Inter.)	B	5 (9)
	Deschutes (eastside)	Intermediate	B	6 (4)
	Klickitat River	Large	B	5 (7)
	Fifteen Mile Creek	Intermediate	C	3 (5)
	Rock Creek	Basic	A	1 (0)
	Crooked River (ext.)	Very Large (?)	A?	
	White Salmon (sthd ext)	Inter. (Basic)	A?	
Yakima River	Upper Yakima River	Very Large	B	10 (11)
	Naches River	Large	B	7 (2)
	Toppenish River	Basic	B	2 (1)
	Satus Creek	Intermediate	B	3 (7)
John Day River	John Day Lower Mainstem	Very Large	B	13 (22)
	John Day North Fork	Large	B	10 (5)
	John Day Upper Mainstem	Intermediate	B	3 (4)
	John Day Middle Fork	Intermediate	B	4 (2)
	John Day South Fork	Basic	B	3 (0)
Umatilla/Walla Walla	Umatilla River	V. Lg. (Large)	B	9 (12)
	Walla-Walla Mainstem	Intermediate	B	5 (6)
	Touchet River	Intermediate	A	3 (3)
	Willow Cr. (sthd ext)			

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Table 3.d: Intrinsic size and complexity ratings for historical populations within the **UPPER COLUMBIA RIVER SPRING CHINOOK ESU**. Organized by Major Population Groupings. Complexity categories: A = Simple linear; B=Dendritic; C= trellis pattern; D= core drainage plus adjacent but separate small tributaries.

Major Population Group	Population	Weighted Area Category	Complexity	
			Category	# MSAs (# Msas)
Eastern Cascades	Wenatchee	Very Large	B	5 (4)
	Methow	Very Large	B	4 (1)
	Entiat	Basic	A	1
	Okanogan River (ext)			1 (3)

Table 3.e: Intrinsic size and complexity ratings for historical populations within the **UPPER COLUMBIA RIVER STEELHEAD ESU**. Organized by Major Population Groupings. Complexity categories: A = Simple linear; B=Dendritic; C= trellis pattern; D= core drainage plus adjacent but separate small tributaries.

Major Population Group	Population	Weighted Area Category	Complexity	
			Category	# MSAs (# Msas)
Eastern Cascades	Wenatchee River	Large	B	5 (13)
	Methow River	Large	B	4 (8)
	Okanogan River	Intermediate	B	10 (24)
	Entiat River	Basic	A	2 (3)

Overlap among ESUs

The following language will be added to the section of appendix B describing the relative distribution of spring chinook and summer chinook in the Wenatchee and Entiat Rivers. The population size designations for these drainages (along with the Methow and the Tucannon) were based on the total amount of weighted habitat within the range identified as spring chinook spawning habitat. Updates to the section are highlighted in italics below.

Summer chinook utilize the Wenatchee River mainstem up through Tumwater Canyon for spawning. Spring chinook are generally confined to the major tributaries to the Wenatchee and the mainstem reach downstream of Lake Wenatchee to Tumwater Canyon.

Spring chinook spawning in the Entiat drainage occurs above river mile 16 of the mainstem and in the lower five miles of a major tributary, the Mad River. Summer chinook spawning extends downstream from approximately river mile 20 to the mouth.

Incorporating Uncertainty into Abundance/Productivity Objectives

Assessments of current abundance and productivity levels are important components of the ICTRT recommended approach to evaluating the status of populations relative to viability objectives. Estimates of the current abundance and productivity of a population will be based on sampling data and therefore will be subject to some level of statistical uncertainty. The level of uncertainty, especially for the estimated productivity of a population, can have a substantial impact relative to achieving targeted risk levels. It is possible to directly incorporate considerations for the level of uncertainty into the risk criteria proposed by the ICTRT. We have developed three alternatives for buffering comparisons of current abundance and productivity for a population against the corresponding risk metrics developed by the ICTRT. We recognize that choices regarding responses to uncertainty include policy considerations, we provide these examples as options to be considered in the recovery planning process.

The following options for directly incorporating parameter uncertainty reflect three major considerations: the desirability for relative simplicity in expressing criteria; direct comparability with the range viability curves we have provided for categorizing population risk (1%, 5% and 25%); and adjustments should be higher as a function of relative uncertainty and risk levels

Table 4 . *Alternative approaches for directly incorporating uncertainty into quantitative assessments of current status. Option A - simple probability based buffer, Option B1 two variations on a dual test approach designed to minimize the chance that the risk level being estimated is actually HIGH.*

Option	**Very Low Risk**	**Low Risk**	**Moderate Risk**
A. Simple Probability Buffer	No less than **an 85% (approx. 1 stnd. error)** chance of being above the **1**% viability curve.	No less than **an 85% (approx. 1 stnd. error)** chance of being above the **5**% viability curve.	No less that a 50% probability of being above the **25%** viability curve
B.1 Dual Comparison: tolerance test to minimize chance that risk is actually High	No less that a 50% probability of being above the **1%** viability curve AND No more than a **1 in 100 (1%)** chance that the actual risk level exceeds **25%**	No less that a 50% probability of being above the **5%** viability curve AND No more than **a 1 in 20 (5%)** chance that the actual risk level exceeds **25%**	No less that a 50% probability of being above the **25%** viability curve
B.2 Dual Comparison: tolerance test to minimize chance that risk is actually High	No less that a 50% probability of being above the **1%** viability curve AND No more than a **1 in 100 (1%)** chance that the actual risk level exceeds **10%**	No less that a 50% probability of being above the **5%** viability curve AND No more than **a 1 in 20 (5%)** chance that the actual risk level exceeds **10%**	No less that a 50% probability of being above the **25%** viability curve

The first option requires that the there be a relatively high likelihood that the risk level being estimated for a particular population actually exceeds a particular threshold before the population can be rated at the corresponding risk level.

The two alternative options (B1 and B2), are designed to be more responsive to the chance that the productivity level is being significantly overestimated. B1 is responsive to the chance that the value is actually below the 25% curve threshold. B2 is more precautionary - being based on the probability that the actual risk is greater than 10%. Both the B1 and B2 options are more sensitive to the level of standard error in the estimates - requiring proportionally more of a buffer when sampling uncertainty is relatively high.

Applying the Uncertainty Adjustments

Under the assumption that variation about mean productivity and abundance follows a log normal distribution, an adjustment factor corresponding to a desired probability of exceeding the target curve can be calculated using the sample standard error:

$$\text{Factor} = \exp(\text{ t value (pct, df)} * \text{SE})$$

The t-values for a given application can be obtained from a standard table (one tailed probability level). For example, for a sample size of 10, the t value corresponding to a 5% probability 1.81.

The relative effects of the options for incorporating uncertainty in estimates of current productivity will depend upon the level of variation associated with a particular estimate (as measured by the sample standard error) and the characteristics of the viability curves for the particular population. The following example (figure 4) illustrates the potential effect of using the alternative approaches for directly incorporating uncertainty associated with productivity estimates. The example is based upon the viability curves for a Very Large population within the Upper Columbia Spring Chinook ESU and includes a range of sample standard errors reflecting the levels calculated from recent data series for interior basin populations.

Figure 5 is a graphical representation of the current status of a hypothentical population relative to the 5% viability curve incorporating an uncertainty buffer (option B1). The figure depicts a population that just meets the dual test provided in option B1. . The error bar is sized using the approach described above so that the lower end corresponds to a 1 in 20 chance of a lower productivity value. In this example the relative level of uncertainty about the estimate of current productivity is large. As a result, the point estimate of productivity must exceed the 5% curve in order to meet the second test - no more than a 1 in 20 chance that the actual estimate is below the 25% risk curve.

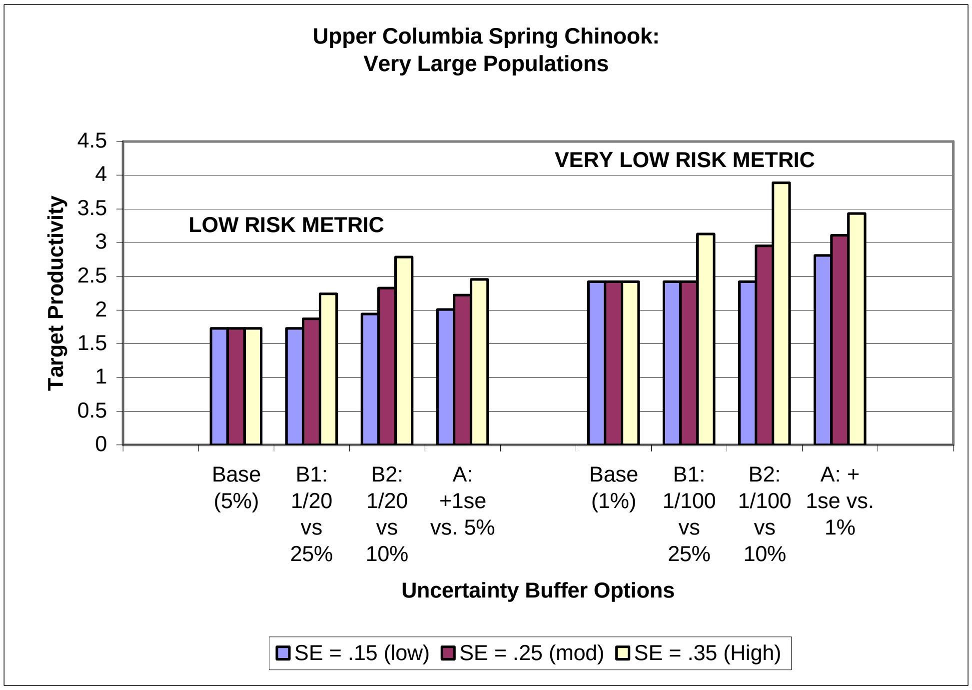

Figure 3. Example of the effects of alternative uncertainty buffers on the minimum productivity required at threshold abundance levels.

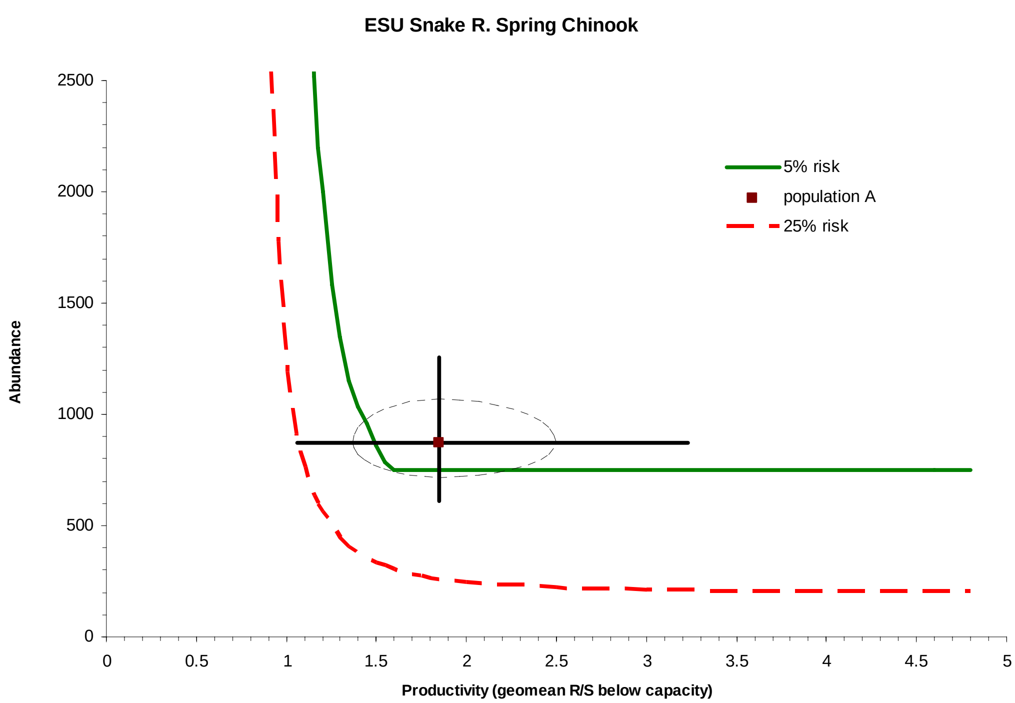

Figure 4. Example illustrating the minimum productivity required relative to the 5% risk level using uncertainty option B1 (point estimate must exceed 5% curve, no more than a 1 in 20 chance that the value being estimated is actually below the 25% risk curve. Error bars represent the 90% confidence limits on the point estimate. Ellipse depicts one standard error about the point estimate.

<u>Snake River Fall chinook Population Viability Criteria</u>

The July 2005 ICTRT Viability Report described the basis for a set of criteria for assessing viability at the population level for listed chinook and steelhead. Detailed applications of those criteria to steelhead and yearling type chinook ESUs were also provided. Snake River fall chinook exhibit important life history differences from yearling chinook and steelhead. Snake River fall chinook spawned primarily in large mainstem reaches and the dominant juvenile life history pattern was for subyearling migration. The ICTRT has adapted the same general population level criteria to apply to Snake River Fall chinook.

<u>Abundance and Productivity Criteria</u>
We calculated a viability curve for Snake River fall chinook following the same analytical steps we applied to yearling chinook and steelhead ESUs. We calculated variance and one year lag autocorrelation statistics for reconstructed brood year spawners and natural returns for 1978-2003. We used a grid-search algorithm to develop a set of viability curves for Snake River fall chinook (Fig. 5) corresponding to projected risk levels of 25%, 10%, 5% and 1% at 100 years.

We established a minimum abundance threshold for fall chinook consistent with the general abundance/productivity objectives summarized in the July 2003 ICTRT Viability draft report. ***We are recommending a minimum abundance threshold of 3,000 natural origin spawners for the extant Snake River fall chinook population. No fewer than 2,500 of those natural origin spawners should be distributed in mainstem Snake River habitat.***

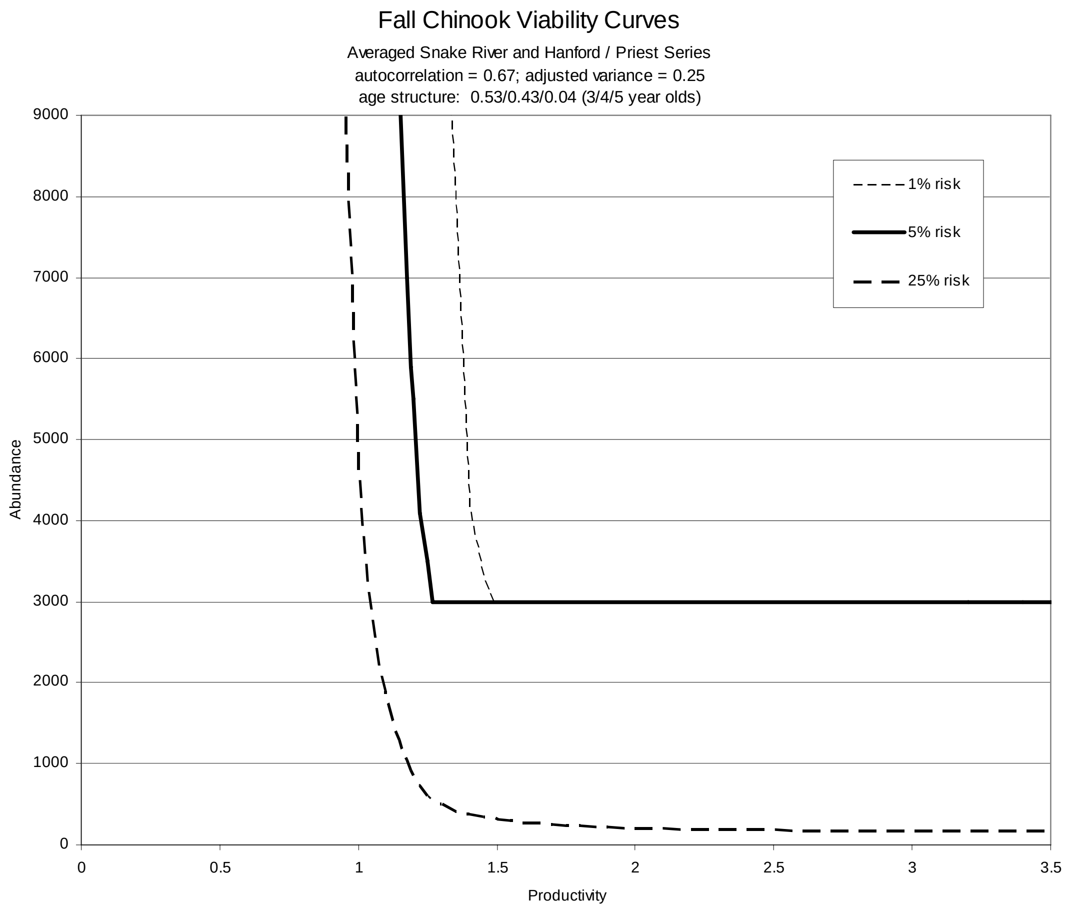

Figure 5. ***Viability curves for Snake River Fall chinook.***

The abundance threshold for Snake River fall chinook is based on the Bevan Team recommendation for "…an eight year (approximately 2 generation) geometic mean of at least 2,500 natural origin spawners in the mainstem Snake River annually." (NMFS, 1995). The Bevan Team specifically did not address spawning/rearing areas in the lower mainstems of major tributaries in setting that objective - stating that "..a lack of information precludes setting escapement objectives at this time." It is likely that lower reaches in the Clearwater, the Grande Ronde and the Tucannon River had the potential to support 500 or more spawners based on physical habitat availability. Fall chinook spawners have been observed in all three areas in recent years (Milks et. al, 2005). Preliminary information from scale sampling and pit tag experiments indicates that natural production of fall chinook in the lower Clearwater may exhibiting a complex life history pattern including overwintering in mainstem habitat before outmigrating to the sea the following spring.

Spatial Structure and Diversity Criteria

The basic objectives for spatial structure and diversity as outlined in the July ICTRT draft viability report apply to Snake River fall chinook. The July draft included specific examples corresponding to a range of risk levels for each individual SSD criteria as well as an approach for integrating across the criteria to arrive at a cumulative population risk rating. The examples were based on yearling chinook and steelhead life history patterns - one or more years of freshwater residence before migrating to the ocean. Several of the metrics used to evaluate against particular SSD criteria involved a measure of population structure based on a historical habitat potential analysis developed expressly for yearling chinook and steelhead. The details of that analysis do not directly apply to the relationship between habitat conditions and spawning/rearing use by Snake River fall chinook. The ICTRT has developed the following approach to identify major and minor spawning aggregations for Snake River fall chinook.

The current fall chinook run is predominately associated with Snake River mainstem habitat between the upper end of the Lower Granite Dam reservoir (near Asotin, Washington)and Hells Canyon Dam. That section of the Snake River mainstem is approximately 163 km in length and can be classified into three distinct reaches based on physical characteristics (Groves and Chandler, 1999). The uppermost reach, from Hells Canyon dam downstream to the mouth of the Salmon River, is characterized by a relatively narrow channel with short, deep pools interspersed with rapids. The middle reach, between the Salmon and Grand Ronde River confluences, widens considerably from a relatively narrow canyon section at its upper end and is characterized by lower gradients. Flows in this reach are augmented by the inflow from the Salmon River drainage. The lowest of the three mainstem reaches extends from the confluence with the Grand Ronde to the upper end of Lower Granite Pool. This reach is characterized by a wide channel with low shorelines, deep pools and relatively few rapids. Flow and turbidity are the most variable in this reach.

We evaluated recent redd distribution data in the context of the physical conditions described above. Redd distributions indicate a consistent gap (encompassing the middle reach as described above) in mainstem spawning between the confluences with the Salmon and Grand Ronde Rivers. Based on the distribution of physical habitat characteristics and the patterns in redd deposition, we defined two historical major spawning areas (MASAs) in the mainstem Snake River upstream of the Lower Granite Reservoir. One mainstem MASA extends from the confluence of the Clearwater River upstream to the confluence of the Salmon River. The second mainstem MASA extends from the confluence of the Salmon River upstream to the general vicinity of Hells Canyon Dam. We concluded that each of these mainstem reaches has the physical capacity to support a minimum of 500 spawners (extrapolated from habitat analyses in Connor et. al, 2001 and Groves & Chandler, 1999). Historically, there may have been an additional relatively contiguous reach capable of supporting spawning in the lower section of the Snake mainstem now inundated by the three lowermost Snake River dams.

The lower reaches of the five major Snake River tributaries entering the mainstem below Hells Canyon dam have been surveyed for fall chinook spawning in recent years. Significant numbers of redds have been located in three tributaries (the Clearwater, Tucannon and Grand Ronde River). Based on physical conditions and current redd densities, we conclude that the all three of these lower tributary reaches should be considered as MASAs in assessing the Snake River fall chinook population status.

Although the core spawning area for this population was the mainstem, the alternative spawning locations in the lower mainstems of tributary rivers provide alternative sources of production when mainstem conditions are poor (e.g., low flows and/or high turbidity).
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> ***Based on these evaluations, the extant Snake River spring chinook population includes five MASAs: the two mainstem mainstem reaches described above along with the lower reaches of the Clearwater, Grand Ronde and Tucannon Rivers. The lower reaches of the Imnaha and Salmon Rivers may have supported relatively low levels of fall chinook spawning and are considered part of the upper mainstem MASA.***

Literature cited

Anon, 2002. Fall chinook salmon spawning ground surveys in the Snake River basin upriver of Lower Granite Dam, 2002. Annual Rept. to Bonneville Power Administration. USFWS, Nez Perce Tribe Fisheries Dept., & Idaho Power Company. Sept. 2003. 49 p.

Connor, WP, A.P. Garcia, A.H. Connor, E.O. Garton, P.A. Groves and J.A. Chandler. 2001. Estimating the carrying capacity of the Snake River for fall chinook salmon redds. Northwest Science. 75(4): 363-371.

Dauble, DD, T.P Hanrahan, D.R. Geist and M.J Parsley. Impacts of the Columbia River hydroelectric system on main-stem habitats of fall chinook salmon. N.Amer. J. Fish. Mgmt. 23:641-659.

Groves, P.A. & J.A. Chandler. 1999. Spawning habitat used by fall chinook salmon in the Snake River. No. Amer. J. Fisheries Management. 19:912-922.

Milks, D., Varney, M, Schuck, M. and Sands, N. J. 2005. Lyons Ferry hatchery evaluation fall chinook salmon annual report: 2001 and 2002. Rept. to USFWS Lower Snake River Compensation Plan Office. April 2005. 100 p.

National Marine Fisheries Service. (1995). Proposed Recovery Plan for Snake River Salmon. U.S. Dept. of Commerce. March, 1995.

Attachment E:

Summaries of Population Characteristics By Major Population Groupings for Interior Columbia Basin Chinook and Steelhead ESUs.

Revised ESU summary tables (12/23/2005)

Salmonid population structure is hierarchical, from species to sub-population, reflecting varying degrees of exchange of individuals. Two levels in this hierarchy have been formally defined for recovery planning efforts ESUs and populations A population is defined as a group of individuals that are demographically independent from other such groups over an 100-year time period. "Major population groupings" are groups of populations that share similarities within the ESU. They are defined on the basis of genetic, geographic (hydrographic), and habitat considerations (McClure et al. 2003). These major population groupings are analogous to "strata" as defined by the Lower Columbia-Upper Willamette TRT and "geographic regions" described by the Puget Sound TRT. The ICTRT has developed draft viability criteria for each of these three levels.

Achieving the MPG level criteria across groupings would generally ensure that populations are functioning across a range of physical and ecological settings reflective of the historical ESU, thereby supporting the expression of genetic and phenotypic diversity. ESUs with only one population or MPG may require more stringent population or MPG criteria to be at low risk.

A summary of population characteristics organized by MPGs within specific ESUs is provided in the following section. Information on a set of key indicators of diversity and spatial complexity at the population level are summarized for each grouping.

Dominant ecoregions - the tributary reaches associated with individual populations can fall within different major ecoregions. Ecoregions represent provincial level differences in vegetation, lithography and elevation.

Life History types (Adults). Differences in adult return timing are generally related to flow and temperature conditions conducive to spawning and incubation requirements. Although multiple adult timing patterns are present within some populations, between population diversity is an important consideration.

Spawning Habitat Quantity: (expressed as kilometers weighted to high quality equivalents). Some MPGs historically included a significant proportion of large and complex populations. MPG viability criteria highlight the need to consider these populations in recovery scenarios.

Median Spawning Elevation (based on intrinsic potential analysis): Adaptation to temperature/precipitation levels can be an important component of diversity within ESUs. Elevation is generally considered a good surrogate for precipitation and temperature. Meeting the MPG population criteria described above would maintain viable populations across the historical range in elevation associated with each ESU (see attached figures).

Valley/Stream Width Ratio: Tributary reaches within unconfined wide valleys provide relatively stable, complex habitats for juvenile rearing (summer and winter phases). The presence of a significant amount of such habitat within the freshwater rearing area associated with a particular population promotes the expression of alternative juvenile life histories.

Table E-1: Upper Columbia River Spring Chinook ESU population characteristics.

Major Population Group	Population	Weighted Area Category	Dominant Ecoregion	Life History (adults)	Median Spawning Elev.	Valley Habitat (prop.)
Eastern Cascades	Wenatchee	Very Large	North Cascades	Spring	590	.38
	Methow	Very Large	North Cascades	Spring	650	.35
	Entiat	Basic	North Cascades	Spring	470	.33
	Okanogan River (ext)					

Table E-2: Summary of population characteristics, organized by Major Population Groupings.

Major Population Group	Population	Weighted Area Category	Dominant Ecoregion	Life History (adults)	Median Spawning Elev.	Valley Habitat (prop.)
Lower Snake	Tucannon R.	Intermediate	Columbia Plateau	Spring	730	.59
	Asotin R.	Basic	Columbia Plateau	Spring	580	.33
Grande Ronde/Imnaha	Lostine/Wallowa R.	Large	Blue Mountains	Spring	990	.61
	Upper Grande Ronde	Large	Blue Mountains	Spring	1000	.50
	Catherine Creek	Large	Blue Mountains	Spring	810	.90
	Imnaha R. Mainstem	Intermediate	Blue Mountains	Spring/Sum	970	.26
	Minam R.	Intermediate	Blue Mountains	Spring	970	.19
	Wenaha R.	Intermediate	Blue Mountains	Spring	620	.15
	Big Sheep Cr.	Basic	Idaho Batholith	Spring	950	.36
	Lookingglass Cr.	Basic	Blue Mountains	Spring	790	.25
South Fork Salmon	South Fk Mainstem	Large	Idaho Batholith	Summer	1260	.13
	Secesh R.	Intermediate	Idaho Batholith	Summer	1740	.46
	East Fk/Johnson Cr.	Large	Idaho Batholith	Summer	1540	.34
	Little Salmon R.	Inter. (Basic)	Blue Mountains	Spring/Sum	800	.09
Middle Fork Salmon	Big Creek	Large	Idaho Batholith	Spring/Sum	1410	.10
	Bear Valley	Intermediate	Idaho Batholith	Spring	1950	.85
	Upper Mainstem MF	Intermediate	Idaho Batholith	Spring	1710	.20
	Chamberlain Cr.	Inter. (Basic)	Idaho Batholith	Spring	1460	.17
	Camas Creek	Basic	Idaho Batholith	Spring	1580	.19
	Loon Creek	Basic	Idaho Batholith	Spring/Sum	1530	.18
	Marsh Creek	Basic	Idaho Batholith	Spring	1990	.76
	Lower Mainstem MF	Basic	Idaho Batholith	Spring	1160	.04
	Sulphur Creek	Basic	Idaho Batholith	Spring	1750	---
Upper Salmon	Lemhi	Very Large	Middle Rockies	Spring	1700	.78
	Lower Mainstem	Very Large	Blue Mountains	Spring/Sum	1570	.24
	Pahsimeroi	Large	Middle Rockies	Summer	1540	.89
	Upper Sal. East Fk	Large	Middle Rockies	Spring/Sum	1790	.43
	Upper Salmon Main	Large	Idaho Batholith	Spring	2080	.88
	Panther Cr (ext)	Intermediate	Idaho Batholith	Spring	1430	.14
	Valley Cr.	Basic	Idaho Batholith	Spring	1970	.91
	Yankee Fork	Basic	Idaho Batholith	Spring	1920	.40
	North Fork Salmon	Basic	Idaho Batholith	Spring	1220	.15

Table E-3: Upper Columbia River Steelhead ESU population characteristics.

Major Population Group	Population	Weighted Area Category	Dominant Ecoregion	Life History (adults)	Median Spawning Elev.
Eastern Cascades	Wenatchee River	Large	North Cascades	Summer A	610
	Methow River	Large	North Cascades	Summer A	670
	Okanogan River	Intermediate		Summer A	600
	Entiat River	Basic	North Cascades	Summer A	490
	Crab Creek			Resident??	

Table E-4. Snake River Steelhead ESU population characteristics. Organized by Major Population Groupings.

Major Population Grouping	Population	Weighted Area Category	Dominant Ecoregion	Life History (adults)	Median Spawning Elev.
Lower Snake	Tucannon R	Intermediate	Columbia Plateau	A type	560
	Asotin R.	Inter. (Basic)	Columbia Plateau	A type	500
Grande Ronde	Upp. Grande Ronde	Large	Blue Mountains	A type	1020
	Wallowa River	Intermediate	Blue Mountains	A type	360
	Lower Grande Ronde	Intermediate	Blue Mountainis	A type	780
	Joseph Creek	Intermediate	Blue Mountains	A type	970
Imnaha River	Imnaha River	Intermediate	Blue Mountains	A type	990
Clearwater River	Lower Mainstem	Large	Northern Rockies	A type	580
	Lochsa River	Large	Idaho Batholith	B type	1100
	Selway River	Large	Idaho Batholith	B type	1060
	South Fork	Intermediate	Idaho Batholith	???	1240
	Lolo Creek	Basic		A&B	930
			Northern Rockies		
	North Fork (blocked)	Very Large		---	950
			Idaho Batholith		
Salmon River	Upper Middle Fork	Large	Idaho Batholith	B type	1780
	Lower Middle Fork	Large	Idaho Batholith	B type	1590
	Lemhi	Intermediate	Middle Rockies	A type	1740
	Upper Salmon East Fk	Intermediate	Idaho Batholith	A type	1770
	Upper Salmon Mainstem	Intermediate	Idaho Batholith	A type	1990
	Chamberlain Cr.	Inter. (Basic)	Idaho Batholith	B type	1470
	Pahsimeroi River	Intermediate	Middle Rockies	A type	1720
	Panther Cr	Intermediate	Idaho Batholith	A type	1680
	Little Salmon River	Inter. (Basic)	Blue Mountains	A type	770
	South Fork	Intermediate	Idaho Batholith	B type	1330
	Secesh R.	Basic	Idaho Batholith	B type	1740
	North Fork	Basic	Idaho Batholith	A type	1350
Hells Canyon Tributaries	Wild Horse/Powder R.	Note: Core spawning areas for this population are blocked to anadromous migration.	Blue Mountains	A type	540

Table E-5: Middle Columbia Steelhead ESU population characteristics. Organized by Major Population Groupings.

Major Population Group	Population	Weighted Area Category	Dominant Ecoregion	Life History (adults)	Median Spawning Elev.
Eastern Cascades	Deschutes (westside)	Large (Inter)	Blue Mountains	Summer	820
	Klickitat River	Large	Eastern Cascades	Sum & Win	640
	Deschutes (eastside)	Intermediate	Columbia Plateau	Summer	610
	Fifteen Mile Creek	Intermediate	Eastern Cascades	Winter	380
	Rock Creek	Basic	Eastern Cascades	Summer	400
	White Salmon (sthd ext)	Int. (Basic)	Eastern Cascades	Summer??	520
Yakima River	Upper Yakima River	Very Large	Columbia Plateau	Summer	680
	Naches River	Large	Eastern Cascades	Summer	800
	Toppenish River	Basic	Columbia Plateau	Summer	540
	Satus Creek	Intermediate	Columbia Plateau	Summer	540
John Day River	John Day Lower Main	Very Large	Blue Mountains	Summer	670
	John Day North Fork	Large	Blue Mountains	Summer	1100
	John Day Upper Main	Intermediate	Blue Mountains	Summer	1080
	John Day Middle Fork	Intermediate	Blue Mountains	Summer	1070
	John Day South Fork	Basic	Blue Mountains	Summer	1220
Umatilla/Walla Walla	Umatilla River	V. Lg. (Lg.)	Columbia Plateau	Summer	570
	Walla-Walla Main	Intermediate	Columbia Plateau	Summer	360
	Touchet River	Intermediate	Columbia Plateau	Summer	510
	Willow Cr. (sthd ext)				